International Rumen Pangenome Program



This project is funded by the following organisations and the Australian Government's Filling the Research Gap Program























Rumen Pangenome Program – an Australian investment in strategic science

Introduce you to the program and our interest in the connection between the host and its ruminal microbial population



- What's it about?
- Structure and international linkages
- The program

Pangenome - what's it about?

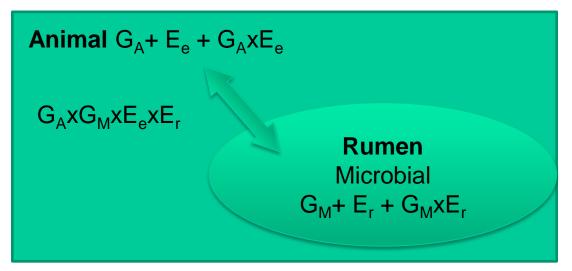
- The full complement of genes in a species
- A superset of all the genes in all the strains of a species
- Reducing methane
 - Challenge extend the pangenome concept to link the host genome to its ruminal microbiome

Why?

To maximise our impact on methane emissions and productivity we have to optimise G x E x M

Understand genes influencing efficiency:

- within the host
- within the microbiome
- between the host and microbiome (more generally, the gastrointestinal tract).



Animal
$$G_A + E_e$$

Microbial
$$G_M + E_r$$

G_A – animal G

E_e – external E

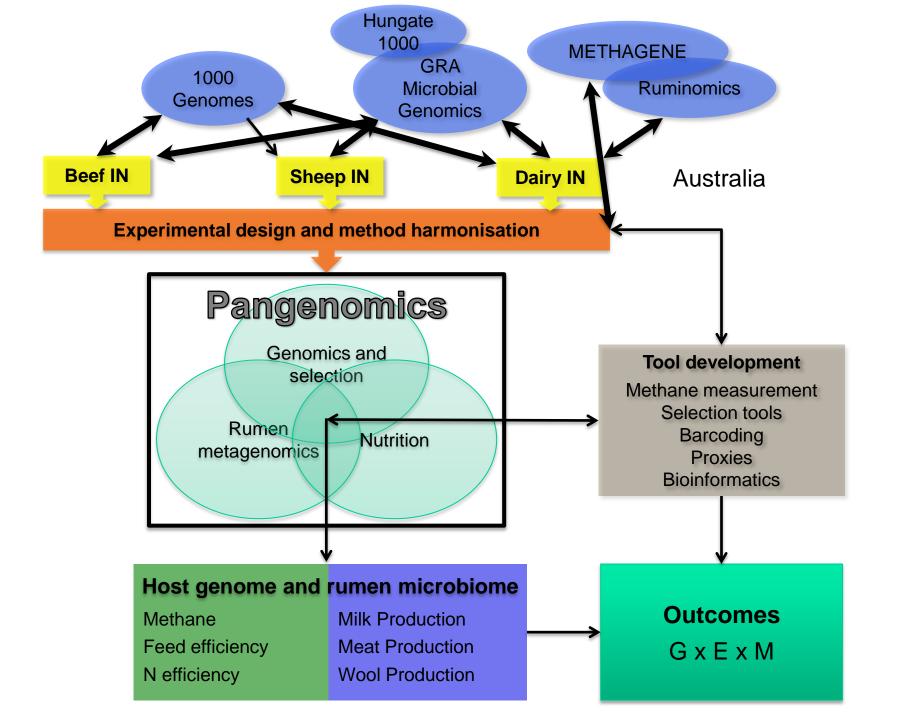
G_M – microbial G

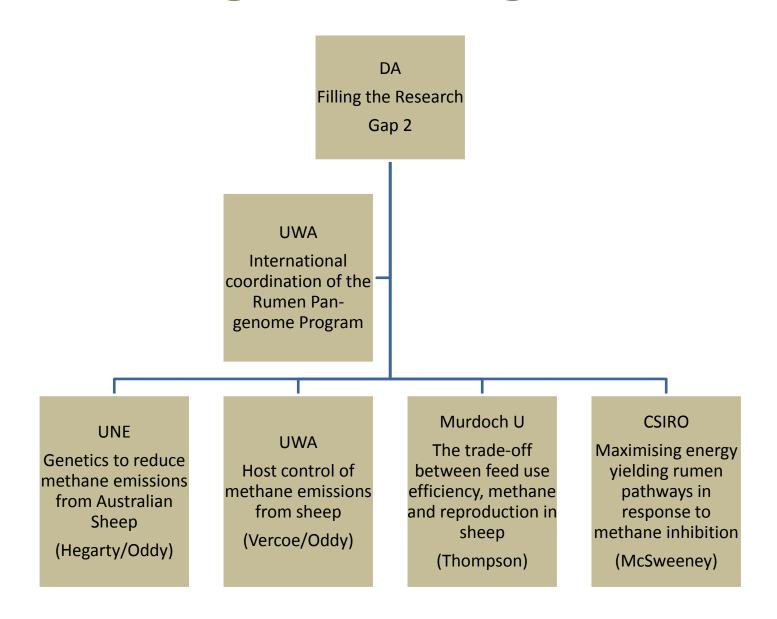
E_r – rumen E

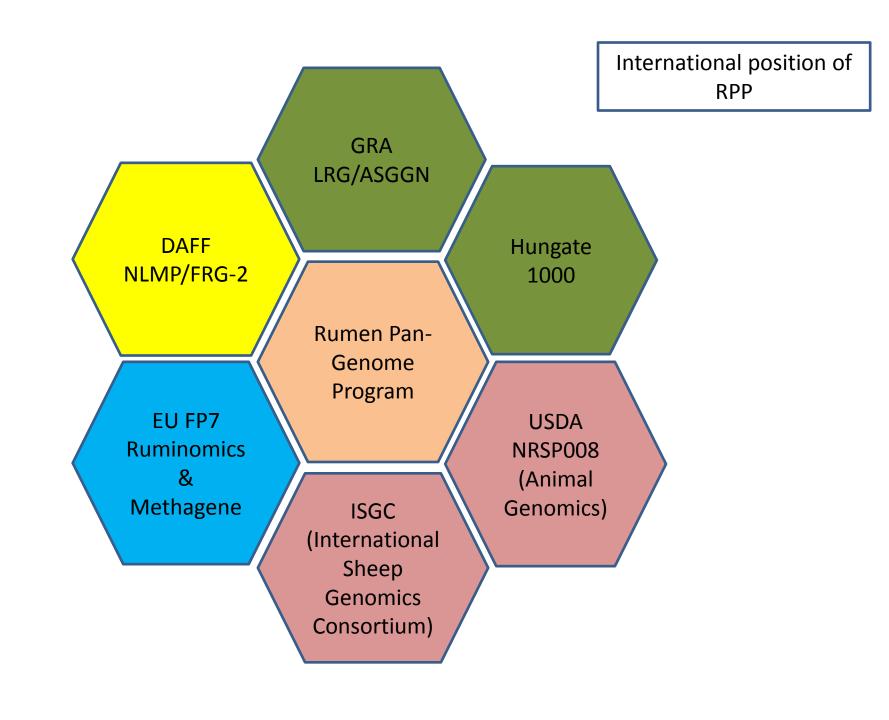
Maybe we should be thinking more along the lines of

Animal
$$P = G_{Pan} + E_{pan}$$

What are we missing out on?







A coordinated multidisciplinary programme designed to:

- Develop greater understanding of the 'pangenome' of ruminants and their microbes
- Identify 'pangenomic' factors affecting the breeding and management of ruminants to lower methane and improve production
- Link to other global initiatives to better understand host/microbe interactions

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